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OM protein - protein search, using sw model

Run on: March 6, 2002, 13:35:19 ; Search time 14.19 Seconds
(without alignments)
1024.463 Million cell updates/sec

Title: US-09-405-504A-25
Perfect score: 3372
Sequence: 1 MRAPGAGAAVVSVLALLWLL.....HYLPLNEAVYTRICSGAPAL 646

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3372	100.0	646	US-09-232-200-25	Sequence 25, Appl
2	3372	100.0	646	US-09-232-200-32	Sequence 32, Appl
3	3372	100.0	646	US-09-232-200-38	Sequence 38, Appl
4	3372	100.0	646	US-09-232-200-43	Sequence 43, Appl
5	3372	100.0	646	US-09-232-200-47	Sequence 47, Appl
6	3372	100.0	646	US-09-232-197-25	Sequence 25, Appl
7	3372	100.0	646	US-09-232-197-32	Sequence 32, Appl
8	3372	100.0	646	US-09-232-197-38	Sequence 38, Appl
9	3372	100.0	646	US-09-232-197-43	Sequence 43, Appl
10	3372	100.0	646	US-09-232-197-47	Sequence 47, Appl
11	3062	90.8	646	US-09-232-200-59	Sequence 59, Appl
12	3062	90.8	646	US-09-232-197-59	Sequence 59, Appl
13	3057	90.7	646	US-09-232-200-92	Sequence 92, Appl
14	3057	90.7	646	US-09-232-197-92	Sequence 92, Appl
15	3054	90.6	646	US-09-232-200-33	Sequence 33, Appl
16	3054	90.6	646	US-09-232-200-65	Sequence 65, Appl
17	3054	90.6	646	US-09-232-197-33	Sequence 33, Appl
18	3054	90.6	646	US-09-232-197-65	Sequence 65, Appl
19	2119	62.8	643	US-09-232-200-27	Sequence 27, Appl
20	2119	62.8	643	US-09-232-200-41	Sequence 41, Appl
21	2119	62.8	643	US-09-232-200-53	Sequence 53, Appl
22	2119	62.8	643	US-09-232-197-27	Sequence 27, Appl
23	2119	62.8	643	US-09-232-197-41	Sequence 41, Appl
24	2119	62.8	643	US-09-232-197-53	Sequence 53, Appl
25	2114.5	62.7	632	US-09-232-200-34	Sequence 34, Appl
26	2114.5	62.7	632	US-09-232-200-39	Sequence 39, Appl
27	2114.5	62.7	632	US-09-232-197-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-09-232-200-25

; Sequence 25, Application US/09232200A

; Patent No. 6288213

; GENERAL INFORMATION:

; APPLICANT: Stahl, Andreas

; APPLICANT: Hirsch, David J.

; APPLICANT: Lodish, Harvey F.

; APPLICANT: Gimeno, Ruth E.

; APPLICANT: Tartaglia, Louis A.

; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS

; FILE REFERENCE: WHI97-21P3MB

; CURRENT APPLICATION NUMBER: US/09/232,200A

; CURRENT FILING DATE: 1999-01-14

; EARLIER APPLICATION NUMBER: 60/071,374

; EARLIER FILING DATE: 1998-01-15

; EARLIER APPLICATION NUMBER: 60/093,491

; EARLIER FILING DATE: 1998-07-20

; EARLIER APPLICATION NUMBER: 60/110,941

; EARLIER FILING DATE: 1998-12-04

; NUMBER OF SEQ ID NOS: 105

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 25

; LENGTH: 646

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-232-200-25

Query Match 100.0%; Score 3372; DB 4; Length 646;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGAGAAVVSVLALLWLLGLPWTWSAAAALGVYVGGWRFRIIVCKTARRDLFGLSV 60

Db 1 MRAPGAGAAVVSVLALLWLLGLPWTWSAAAALGVYVGGWRFRIIVCKTARRDLFGLSV 60

QY 61 LIRVRLRRHORAGHTIPRIFQAVVORQPERLALVDAGTGCWTFQAQLDAYSNANLNF 120

Db 61 LIRVRLRRHORAGHTIPRIFQAVVORQPERLALVDAGTGCWTFQAQLDAYSNANLNF 120

QY 121 RQLGFAPGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVLNRRREPLAFCLGTSAGAKALI 180

Db 121 RQLGFAPGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVLNRRREPLAFCLGTSAGAKALI 180

QY 181 FGGEMVAAEVSGHLGKSLIKFCSDGLGPEGLIPDTHLLDPLLLKEASTAPLAQIPSKGM 240

Db 181 FGGEMVAAEVSGHLGKSLIKFCSDGLGPEGLIPDTHLLDPLLLKEASTAPLAQIPSKGM 240

QY 241 DDRLFYITSGTTGLPKAAIIVHSHRYRMAAFGHAYRMAQADVLDCLPLYHSAGNIIC 300

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Db 241 DDLRFYIYSGTGLPKAAIVVHSRYRMAAFGHAYRMAQADVLYDCLPLYHSAGNIIG 300
QY 301 VGOCIIYGLTVLVRKFKFSASRFDWDCIKYNCTVVOYIGEICRYLLKQPVREARRHRVRL 360
Db 301 VGOCIIYGLTVLVRKFKFSASRFDWDCIKYNCTVVOYIGEICRYLLKQPVREARRHRVRL 360
QY 361 AVGNGLRPAIWEETFERFVGVRQIGEFYGAECNCISIANMDKGVSGFNSRLPHVPIR 420
Db 361 AVGNGLRPAIWEETFERFVGVRQIGEFYGAECNCISIANMDKGVSGFNSRLPHVPIR 420
QY 421 LKVNEDTMELLRDAQGLCIPCOAGPEGLLVGOINQODPLRRFDGVVSESATSKKIAHSV 480
Db 421 LKVNEDTMELLRDAQGLCIPCOAGPEGLLVGOINQODPLRRFDGVVSESATSKKIAHSV 480
QY 481 FSKGDSAYLSGDVLMDELGYMYFRDRSGDTFRWRGENVSTTEVEGVLSRLLGQTDVAVY 540
Db 481 FSKGDSAYLSGDVLMDELGYMYFRDRSGDTFRWRGENVSTTEVEGVLSRLLGQTDVAVY 540
QY 541 GVAVPGVEGKAGMAAVADPHSLDDPNNAIYOELQKVLAPYARPIFLRLLPOVDTTGTFKIQ 600
Db 541 GVAVPGVEGKAGMAAVADPHSLDDPNNAIYOELQKVLAPYARPIFLRLLPOVDTTGTFKIQ 600
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Db 601 KTRLOREGDPROTSDRLFFLDLKQGHYLPNEAVYTRICSGAFAL 646
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RESULT 2

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US-09-232-200-32
; Sequence 32, Application US/092322200A
; Patent No. 6288213
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21D3MB
; CURRENT APPLICATION NUMBER: US/09/232,200A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-200-32
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Query Match 100.0%; Score 3372; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MRAPGAGAASVVSALLWLLGLPWTWSAAAALGVYVSGGWRFLRIVCKTARRDLFGLSV 60
QY 61 LIRVLELRHORAGHTTIPRIFOAVQORPERLALVDAGTGCWTFQAOLDAYSNAVANLF 120
Db 61 LIRVLELRHORAGHTTIPRIFOAVQORPERLALVDAGTGCWTFQAOLDAYSNAVANLF 120
QY 121 RQLGFAPGDVVAIFLEGRPEFVGLWLGLAKAGMEALLNVLNRRPLAFCLGTSGAKALI 180
Db 121 RQLGFAPGDVVAIFLEGRPEFVGLWLGLAKAGMEALLNVLNRRPLAFCLGTSGAKALI 180
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Db 181 FGEWMAAAVEVSGHLGKSLIKFCSDGLPEGILPDLHLLDPLLEKEASTAPLAQIPSKGM 240
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Db 241 DDLRFYIYSGTGLPKAAIVVHSRYRMAAFGHAYRMAQADVLYDCLPLYHSAGNIIG 300
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Db 301 VGOCIIYGLTVLVRKFKFSASRFDWDCIKYNCTVVOYIGEICRYLLKQPVREARRHRVRL 360
QY 361 AVGNGLRPAIWEETFERFVGVRQIGEFYGAECNCISIANMDKGVSGFNSRLPHVPIR 420
Db 361 AVGNGLRPAIWEETFERFVGVRQIGEFYGAECNCISIANMDKGVSGFNSRLPHVPIR 420
QY 421 LKVNEDTMELLRDAQGLCIPCOAGPEGLLVGOINQODPLRRFDGVVSESATSKKIAHSV 480
Db 421 LKVNEDTMELLRDAQGLCIPCOAGPEGLLVGOINQODPLRRFDGVVSESATSKKIAHSV 480
QY 481 FSKGDSAYLSGDVLMDELGYMYFRDRSGDTFRWRGENVSTTEVEGVLSRLLGQTDVAVY 540
Db 481 FSKGDSAYLSGDVLMDELGYMYFRDRSGDTFRWRGENVSTTEVEGVLSRLLGQTDVAVY 540
QY 541 GVAVPGVEGKAGMAAVADPHSLDDPNNAIYOELQKVLAPYARPIFLRLLPOVDTTGTFKIQ 600
Db 541 GVAVPGVEGKAGMAAVADPHSLDDPNNAIYOELQKVLAPYARPIFLRLLPOVDTTGTFKIQ 600
QY 601 KTRLOREGDPROTSDRLFFLDLKQGHYLPNEAVYTRICSGAFAL 646
Db 601 KTRLOREGDPROTSDRLFFLDLKQGHYLPNEAVYTRICSGAFAL 646
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RESULT 3

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US-09-232-200-38
; Sequence 38, Application US/092322200A
; Patent No. 6288213
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MB
; CURRENT APPLICATION NUMBER: US/09/232,200A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-200-38
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Query Match 100.0%; Score 3372; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MRAPGAGAASVVSALLWLLGLPWTWSAAAALGVYVSGGWRFLRIVCKTARRDLFGLSV 60
QY 61 LIRVLELRHORAGHTTIPRIFOAVQORPERLALVDAGTGCWTFQAOLDAYSNAVANLF 120
Db 61 LIRVLELRHORAGHTTIPRIFOAVQORPERLALVDAGTGCWTFQAOLDAYSNAVANLF 120
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Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRAPGAGAAVSVSLALLWLLGLPWTWSAAAALGVVVGSGWRFLRIYCKTARRDLFGLSV 60

QY 61 LIRVLELRHRRHAGHTIPRIQAVVQORPERLALVDAGTGEQWTFQAOLDAYSNAVANLF 120
DB 61 LIRVLELRHRRHAGHTIPRIQAVVQORPERLALVDAGTGEQWTFQAOLDAYSNAVANLF 120

QY 121 ROLGAPAGDVVAIFLEGPEFVGLWGLAKAGMEAAALLNVNLRREPLAFCLGTSKAKALI 180
DB 121 ROLGAPAGDVVAIFLEGPEFVGLWGLAKAGMEAAALLNVNLRREPLAFCLGTSKAKALI 180

QY 181 FGGEMVAVAEVSCHLGSLLKFCSDGLGPEGILPDTHLLDPLLEKEASTAPLAQIPSKGM 240
DB 181 FGGEMVAVAEVSCHLGSLLKFCSDGLGPEGILPDTHLLDPLLEKEASTAPLAQIPSKGM 240

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DB 241 DDLRFYIYTSGTGLPKAAIVVHSRYRMAAFGHYRMAQADVLYDCLPLYHSAGNIIG 300

QY 301 VGQCLLYGLTVLVRKKSASRFDWDCIKYNTVVOYIGEICRYLLKQPVREARRHRVRL 360
DB 301 VGQCLLYGLTVLVRKKSASRFDWDCIKYNTVVOYIGEICRYLLKQPVREARRHRVRL 360

QY 361 AVGNGLRPAIWEETFERFGVQIGEFYGATECNCSIANMDGKVGSCGFSNRILPHVYPIR 420
DB 361 AVGNGLRPAIWEETFERFGVQIGEFYGATECNCSIANMDGKVGSCGFSNRILPHVYPIR 420

QY 421 LVKVNEDTMELLRDAQGLCIPCOAGEPGLLVQINQODPLRRFDGYSSESATSKIAHSV 480
DB 421 LVKVNEDTMELLRDAQGLCIPCOAGEPGLLVQINQODPLRRFDGYSSESATSKIAHSV 480

QY 481 FSKGDSAYLSGDLVMDDELGYMFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540
DB 481 FSKGDSAYLSGDLVMDDELGYMFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540

QY 541 GVAVPGVEGKAGMAAVADPHSLDPNAYIQELQKVLAPYARPIFLRLPQVDTTGTFTKI 600
DB 541 GVAVPGVEGKAGMAAVADPHSLDPNAYIQELQKVLAPYARPIFLRLPQVDTTGTFTKI 600

QY 601 KTRLQREGFDPRTSDRLFFDLKQGHYLPNEAVYTRICSGAFAL 646
DB 601 KTRLQREGFDPRTSDRLFFDLKQGHYLPNEAVYTRICSGAFAL 646

RESULT 6
US-09-232-197-25
; Sequence 25, Application US/09232197A
; Patent No. 6300096
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; FILE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; CURRENT APPLICATION NUMBER: US/09/232,197A
; EARLIER FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 646
; TYPE: PRN

ORGANISM: Homo sapiens
US-09-232-197-25

Query Match 100.0%; Score 3372; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGAGAAVSVSLALLWLLGLPWTWSAAAALGVVVGSGWRFLRIYCKTARRDLFGLSV 60
DB 1 MRAPGAGAAVSVSLALLWLLGLPWTWSAAAALGVVVGSGWRFLRIYCKTARRDLFGLSV 60

QY 61 LIRVLELRHRRHAGHTIPRIQAVVQORPERLALVDAGTGEQWTFQAOLDAYSNAVANLF 120
DB 61 LIRVLELRHRRHAGHTIPRIQAVVQORPERLALVDAGTGEQWTFQAOLDAYSNAVANLF 120

QY 121 ROLGAPAGDVVAIFLEGPEFVGLWGLAKAGMEAAALLNVNLRREPLAFCLGTSKAKALI 180
DB 121 ROLGAPAGDVVAIFLEGPEFVGLWGLAKAGMEAAALLNVNLRREPLAFCLGTSKAKALI 180

QY 181 FGGEMVAVAEVSCHLGSLLKFCSDGLGPEGILPDTHLLDPLLEKEASTAPLAQIPSKGM 240
DB 181 FGGEMVAVAEVSCHLGSLLKFCSDGLGPEGILPDTHLLDPLLEKEASTAPLAQIPSKGM 240

QY 241 DDLRFYIYTSGTGLPKAAIVVHSRYRMAAFGHYRMAQADVLYDCLPLYHSAGNIIG 300
DB 241 DDLRFYIYTSGTGLPKAAIVVHSRYRMAAFGHYRMAQADVLYDCLPLYHSAGNIIG 300

QY 301 VGQCLLYGLTVLVRKKSASRFDWDCIKYNTVVOYIGEICRYLLKQPVREARRHRVRL 360
DB 301 VGQCLLYGLTVLVRKKSASRFDWDCIKYNTVVOYIGEICRYLLKQPVREARRHRVRL 360

QY 361 AVGNGLRPAIWEETFERFGVQIGEFYGATECNCSIANMDGKVGSCGFSNRILPHVYPIR 420
DB 361 AVGNGLRPAIWEETFERFGVQIGEFYGATECNCSIANMDGKVGSCGFSNRILPHVYPIR 420

QY 421 LVKVNEDTMELLRDAQGLCIPCOAGEPGLLVQINQODPLRRFDGYSSESATSKIAHSV 480
DB 421 LVKVNEDTMELLRDAQGLCIPCOAGEPGLLVQINQODPLRRFDGYSSESATSKIAHSV 480

QY 481 FSKGDSAYLSGDLVMDDELGYMFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540
DB 481 FSKGDSAYLSGDLVMDDELGYMFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540

QY 541 GVAVPGVEGKAGMAAVADPHSLDPNAYIQELQKVLAPYARPIFLRLPQVDTTGTFTKI 600
DB 541 GVAVPGVEGKAGMAAVADPHSLDPNAYIQELQKVLAPYARPIFLRLPQVDTTGTFTKI 600

QY 601 KTRLQREGFDPRTSDRLFFDLKQGHYLPNEAVYTRICSGAFAL 646
DB 601 KTRLQREGFDPRTSDRLFFDLKQGHYLPNEAVYTRICSGAFAL 646

RESULT 7
US-09-232-197-32
; Sequence 32, Application US/09232197A
; Patent No. 6300096
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; FILE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; CURRENT APPLICATION NUMBER: US/09/232,197A
; EARLIER FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04

; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-197-32

Query Match 100.0%; Score 3372; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGAGAAVSLSALLLGLPWTWSAAAALGVVYVSGGWRFLRVCKTARRDLFGLSV 60
DB 1 MRAPGAGAAVSLSALLLGLPWTWSAAAALGVVYVSGGWRFLRVCKTARRDLFGLSV 60

QY 61 LIRVLELRHQRAGHTIPRIFQAVVQROPRLALVDAGTGCWTFQAQLDAYSNVANLF 120
DB 61 LIRVLELRHQRAGHTIPRIFQAVVQROPRLALVDAGTGCWTFQAQLDAYSNVANLF 120

QY 121 RQLGFAPGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180
DB 121 RQLGFAPGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180

QY 181 FGGEMVAAEVSGHLGKSLIKFCSDGLPGLPDLTHLLDPLLEASTAPLAQIPSKGM 240
DB 181 FGGEMVAAEVSGHLGKSLIKFCSDGLPGLPDLTHLLDPLLEASTAPLAQIPSKGM 240

QY 241 DDLRFYIYTSGLTPKAAIVVHSRYRMAAFGHAYRMAAADVLYDCLPLYHSAGNIIG 300
DB 241 DDLRFYIYTSGLTPKAAIVVHSRYRMAAFGHAYRMAAADVLYDCLPLYHSAGNIIG 300

QY 301 VGOCCLYGLTVLVRKKSASRFWDDCIKYNCTVVOYIGEICRYLLKQPVREARRHVR 360
DB 301 VGOCCLYGLTVLVRKKSASRFWDDCIKYNCTVVOYIGEICRYLLKQPVREARRHVR 360

QY 361 AVGNGLRPAIWEETERFVGVRQIGEFYGATECNCSTANMDKGVSCGFNSRLPHVYPIR 420
DB 361 AVGNGLRPAIWEETERFVGVRQIGEFYGATECNCSTANMDKGVSCGFNSRLPHVYPIR 420

QY 421 LKVNEDTMELLRDAQGLCIPCOAGEPGLLVGOINQODPLRRFDGVVSESATSKIAHSV 480
DB 421 LKVNEDTMELLRDAQGLCIPCOAGEPGLLVGOINQODPLRRFDGVVSESATSKIAHSV 480

QY 481 FSKGDSAYLSGDVLYMDELGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540
DB 481 FSKGDSAYLSGDVLYMDELGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540

QY 541 GVAVPGVEGKAGMAAVADPHSLDPNAYIQELQKVLAPYARPIFLRLLPQVDTTGTFTKIQ 600
DB 541 GVAVPGVEGKAGMAAVADPHSLDPNAYIQELQKVLAPYARPIFLRLLPQVDTTGTFTKIQ 600

QY 601 KTRLOREGFDPRTSDRLFFLDLKQGHYLPNEAVYTRICSGAFAL 646
DB 601 KTRLOREGFDPRTSDRLFFLDLKQGHYLPNEAVYTRICSGAFAL 646

RESULT 8
US-09-232-197-38
; Sequence 38, Application US/09232197A
; Patent No. 6300096
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MA
; CURRENT APPLICATION NUMBER: US/09/232.197A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374

; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-197-38

Query Match 100.0%; Score 3372; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGAGAAVSLSALLLGLPWTWSAAAALGVVYVSGGWRFLRVCKTARRDLFGLSV 60
DB 1 MRAPGAGAAVSLSALLLGLPWTWSAAAALGVVYVSGGWRFLRVCKTARRDLFGLSV 60

QY 61 LIRVLELRHQRAGHTIPRIFQAVVQROPRLALVDAGTGCWTFQAQLDAYSNVANLF 120
DB 61 LIRVLELRHQRAGHTIPRIFQAVVQROPRLALVDAGTGCWTFQAQLDAYSNVANLF 120

QY 121 RQLGFAPGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180
DB 121 RQLGFAPGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180

QY 181 FGGEMVAAEVSGHLGKSLIKFCSDGLPGLPDLTHLLDPLLEASTAPLAQIPSKGM 240
DB 181 FGGEMVAAEVSGHLGKSLIKFCSDGLPGLPDLTHLLDPLLEASTAPLAQIPSKGM 240

QY 241 DDLRFYIYTSGLTPKAAIVVHSRYRMAAFGHAYRMAAADVLYDCLPLYHSAGNIIG 300
DB 241 DDLRFYIYTSGLTPKAAIVVHSRYRMAAFGHAYRMAAADVLYDCLPLYHSAGNIIG 300

QY 301 VGOCCLYGLTVLVRKKSASRFWDDCIKYNCTVVOYIGEICRYLLKQPVREARRHVR 360
DB 301 VGOCCLYGLTVLVRKKSASRFWDDCIKYNCTVVOYIGEICRYLLKQPVREARRHVR 360

QY 361 AVGNGLRPAIWEETERFVGVRQIGEFYGATECNCSTANMDKGVSCGFNSRLPHVYPIR 420
DB 361 AVGNGLRPAIWEETERFVGVRQIGEFYGATECNCSTANMDKGVSCGFNSRLPHVYPIR 420

QY 421 LKVNEDTMELLRDAQGLCIPCOAGEPGLLVGOINQODPLRRFDGVVSESATSKIAHSV 480
DB 421 LKVNEDTMELLRDAQGLCIPCOAGEPGLLVGOINQODPLRRFDGVVSESATSKIAHSV 480

QY 481 FSKGDSAYLSGDVLYMDELGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540
DB 481 FSKGDSAYLSGDVLYMDELGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGQTDVAVY 540

QY 541 GVAVPGVEGKAGMAAVADPHSLDPNAYIQELQKVLAPYARPIFLRLLPQVDTTGTFTKIQ 600
DB 541 GVAVPGVEGKAGMAAVADPHSLDPNAYIQELQKVLAPYARPIFLRLLPQVDTTGTFTKIQ 600

QY 601 KTRLOREGFDPRTSDRLFFLDLKQGHYLPNEAVYTRICSGAFAL 646
DB 601 KTRLOREGFDPRTSDRLFFLDLKQGHYLPNEAVYTRICSGAFAL 646

RESULT 9
US-09-232-197-43
; Sequence 43, Application US/09232197A
; Patent No. 6300096
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.

; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WH197-21p3MA
; CURRENT APPLICATION NUMBER: US/09/232,197A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-197-43

Query Match 100.0%; Score 3372; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGAGAAVVSALLLWLLGLPWTWSAAALGVVVGSGGWRFLRIVCKTARRDLFGLSV 60
Db 1 MRAPGAGAAVVSALLLWLLGLPWTWSAAALGVVVGSGGWRFLRIVCKTARRDLFGLSV 60

QY 61 LIRVLELRHQRAGHTIPRIFQAVVQRPERLALVDAGTGEWTFQAOLDAYSNAVANLF 120
Db 61 LIRVLELRHQRAGHTIPRIFQAVVQRPERLALVDAGTGEWTFQAOLDAYSNAVANLF 120

QY 121 RQLGFAPGDVVAIFLEGPEFVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180
Db 121 RQLGFAPGDVVAIFLEGPEFVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180

QY 181 FGGEMVAAVAEVSCHLGLSLKFCSDGLGPEGLPDTLLDPLLEKEASTAPLAQIPSKGM 240
Db 181 FGGEMVAAVAEVSCHLGLSLKFCSDGLGPEGLPDTLLDPLLEKEASTAPLAQIPSKGM 240

QY 241 DDRLFYITSGTTGLPKAAIVVHSRYRMAAFGHAYRMOAADVLYDCLPLYHSAGNIIG 300
Db 241 DDRLFYITSGTTGLPKAAIVVHSRYRMAAFGHAYRMOAADVLYDCLPLYHSAGNIIG 300

QY 301 VGOCLYGLTVLVRKFSASRFWDDCIKYNCTVQYIGEICRYLLKQPVREARRHRVRL 360
Db 301 VGOCLYGLTVLVRKFSASRFWDDCIKYNCTVQYIGEICRYLLKQPVREARRHRVRL 360

QY 361 AVGNGLRPAIWEETFERFGVROIGEFYGATECNCSIANMDGKVGSCGFNSRLPHVYPPIR 420
Db 361 AVGNGLRPAIWEETFERFGVROIGEFYGATECNCSIANMDGKVGSCGFNSRLPHVYPPIR 420

QY 421 LVKVNEDTMELLRDAQGLCIPCOAGBGLLVQINQOQPLRRFDGYSSESATSKIAHSV 480
Db 421 LVKVNEDTMELLRDAQGLCIPCOAGBGLLVQINQOQPLRRFDGYSSESATSKIAHSV 480

QY 481 FSKGDSAYLSGDVLYMDELGYMYFRDRSGDTFRWGENVSTTEVEGVSRLLGOTDVAVY 540
Db 481 FSKGDSAYLSGDVLYMDELGYMYFRDRSGDTFRWGENVSTTEVEGVSRLLGOTDVAVY 540

QY 541 GVAVPGECKAGMAAADPHSLDNPNAIYQELQKVLAPYARPIFLRLLPQVDTTGTFTKIQ 600
Db 541 GVAVPGECKAGMAAADPHSLDNPNAIYQELQKVLAPYARPIFLRLLPQVDTTGTFTKIQ 600

QY 601 KTRLOREGFDPQTSRDLFFLDLKQGHYLPNEAVYTRICSGAFAL 646
Db 601 KTRLOREGFDPQTSRDLFFLDLKQGHYLPNEAVYTRICSGAFAL 646

RESULT 10

US-09-232-197-47
; Sequence 47, Application US/09232197A
; Patent No. 630096
; GENERAL INFORMATION:

; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WH197-21p3MA
; CURRENT APPLICATION NUMBER: US/09/232,197A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-197-47

Query Match 100.0%; Score 3372; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPGAGAAVVSALLLWLLGLPWTWSAAALGVVVGSGGWRFLRIVCKTARRDLFGLSV 60
Db 1 MRAPGAGAAVVSALLLWLLGLPWTWSAAALGVVVGSGGWRFLRIVCKTARRDLFGLSV 60

QY 61 LIRVLELRHQRAGHTIPRIFQAVVQRPERLALVDAGTGEWTFQAOLDAYSNAVANLF 120
Db 61 LIRVLELRHQRAGHTIPRIFQAVVQRPERLALVDAGTGEWTFQAOLDAYSNAVANLF 120

QY 121 RQLGFAPGDVVAIFLEGPEFVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180
Db 121 RQLGFAPGDVVAIFLEGPEFVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALI 180

QY 181 FGGEMVAAVAEVSCHLGLSLKFCSDGLGPEGLPDTLLDPLLEKEASTAPLAQIPSKGM 240
Db 181 FGGEMVAAVAEVSCHLGLSLKFCSDGLGPEGLPDTLLDPLLEKEASTAPLAQIPSKGM 240

QY 241 DDRLFYITSGTTGLPKAAIVVHSRYRMAAFGHAYRMOAADVLYDCLPLYHSAGNIIG 300
Db 241 DDRLFYITSGTTGLPKAAIVVHSRYRMAAFGHAYRMOAADVLYDCLPLYHSAGNIIG 300

QY 301 VGOCLYGLTVLVRKFSASRFWDDCIKYNCTVQYIGEICRYLLKQPVREARRHRVRL 360
Db 301 VGOCLYGLTVLVRKFSASRFWDDCIKYNCTVQYIGEICRYLLKQPVREARRHRVRL 360

QY 361 AVGNGLRPAIWEETFERFGVROIGEFYGATECNCSIANMDGKVGSCGFNSRLPHVYPPIR 420
Db 361 AVGNGLRPAIWEETFERFGVROIGEFYGATECNCSIANMDGKVGSCGFNSRLPHVYPPIR 420

QY 421 LVKVNEDTMELLRDAQGLCIPCOAGBGLLVQINQOQPLRRFDGYSSESATSKIAHSV 480
Db 421 LVKVNEDTMELLRDAQGLCIPCOAGBGLLVQINQOQPLRRFDGYSSESATSKIAHSV 480

QY 481 FSKGDSAYLSGDVLYMDELGYMYFRDRSGDTFRWGENVSTTEVEGVSRLLGOTDVAVY 540
Db 481 FSKGDSAYLSGDVLYMDELGYMYFRDRSGDTFRWGENVSTTEVEGVSRLLGOTDVAVY 540

QY 541 GVAVPGECKAGMAAADPHSLDNPNAIYQELQKVLAPYARPIFLRLLPQVDTTGTFTKIQ 600
Db 541 GVAVPGECKAGMAAADPHSLDNPNAIYQELQKVLAPYARPIFLRLLPQVDTTGTFTKIQ 600

QY 601 KTRLOREGFDPQTSRDLFFLDLKQGHYLPNEAVYTRICSGAFAL 646
Db 601 KTRLOREGFDPQTSRDLFFLDLKQGHYLPNEAVYTRICSGAFAL 646

Db 361 AVGNGLRPAIWEETQREGVQIGEFYGATECNCSTANMDGKVGSCGFNSRILTHVPIR 420
QY 421 LVKVNEDTMELLRDAGCLTIPCQAGPGLLVGOINQODPLRRFDGYVSESATSKKIAHSV 480
Db 421 LVKVNEDTMELLRDAGCLTIPCQAGPGLLVGOINQODPLRRFDGYVSESATSKKIAHSV 480
QY 481 FSKGDSAYLSGDLVMDLGYMYFRDRSGDTFRWRGENVSTTEVEAVLSRLLGQTDVAVY 540
Db 481 FSKGDSAYLSGDLVMDLGYMYFRDRSGDTFRWRGENVSTTEVEAVLSRLLGQTDVAVY 540
QY 541 GVAVPGVEGKAGMAAVADPHSLDPAIYQELQKVLAPYARPIFLRLLPQVDTTGTFKIQ 600
Db 541 GVAVPGVEGKAGMAAVADPHSLDPAIYQELQKVLAPYARPIFLRLLPQVDTTGTFKIQ 600
QY 601 KTRLOREGFDPRTSDRLFLDLKQGHYPLNEAVYTRICSGAFAL 646
Db 601 KTRLOREGFDPRTSDRLFLDLKQGHYPLNEAVYTRICSGAFAL 646

RESULT 15

US-09-232-200-33
; Sequence 33, Application US/09232200A
; Patent No. 6286213
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WH197-21p3MB
; CURRENT APPLICATION NUMBER: US/09/232,200A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-232-200-33

Query Match 90.6%; Score 3054; DB 4; Length 646;
Best Local Similarity 89.5%; Pred. No. 0;
Matches 578; Conservative 30; Mismatches 38; Indels 0; Gaps 0;
QY 1 MRAPGAGAAVSVLALLMLGLPTWTSAAAALGVVGGWRFRIIVCKTARRDLFGLSV 60
Db 1 MRAPGAGTASVALLMLGLPTWTSAAAALGVVGGWRFRIIVCKTARRDLFGLSV 60
QY 61 LIRVLELRHRRAGHTIPRIFQAVVQRPRLALVDAGTCECWTFAQLDAYSNVANLF 120
Db 61 LIRVLELRHRRAGHTIPRIFQAVVQRPRLALVDAGTCECWTFAQLDAYSNVANLF 120
QY 121 ROLGAPGDVVAVIFLEGPEFVGLWGLAKAGMEAAALLNVNLRREPLAFCLGTSCAKALI 180
Db 121 ROLGAPGDVVAVIFLEGPEFVGLWGLAKAGVVAALLNVNLRREPLAFCLGTSCAKALI 180
QY 181 FGGEMVAAYAEVSHGLKSLIKFCSGDLGPEGILPDTHLLDPLLKEASTAPLAQIPSKGM 240
Db 181 YGEMAAAAVAEVSQGLKSLIKFCSGDLGPEGILPDTHLLDPLLKEASTAPLAQIPSKGM 240
QY 241 DDLRFYIYTSGLPKAAIIVVSHRYRMAAFGHAYRMOAADVLYDCLPLYHSAGNIIG 300
Db 241 DDLRFYIYTSGLPKAAIIVVSHRYRMAAFGHAYRMOAADVLYDCLPLYHSAGNIIG 300

QY 301 VQOCLLYGLTVLRRKFSASRFWDDCIKYNCTVVQYIGEICRYLLKQPVREARRHRVRL 360
Db 301 VQOCLLYGLTVLRRKFSASRFWDDCIKYNCTVVQYIGEICRYLLKQPVREARRHRVRL 360
QY 361 AVGNCLRPAIWEETQREGVQIGEFYGATECNCSTANMDGKVGSCGFNSRILTHVPIR 420
Db 361 AVGNCLRPAIWEETQREGVQIGEFYGATECNCSTANMDGKVGSCGFNSRILTHVPIR 420
QY 421 LVKVNEDTMELLRDAGCLTIPCQAGPGLLVGOINQODPLRRFDGYVSESATSKKIAHSV 480
Db 421 LVKVNEDTMELLRDAGCLTIPCQAGPGLLVGOINQODPLRRFDGYVSESATSKKIAHSV 480
QY 481 FSKGDSAYLSGDLVMDLGYMYFRDRSGDTFRWRGENVSTTEVEAVLSRLLGQTDVAVY 540
Db 481 FSKGDSAYLSGDLVMDLGYMYFRDRSGDTFRWRGENVSTTEVEAVLSRLLGQTDVAVY 540
QY 541 GVAVPGVEGKAGMAAVADPHSLDPAIYQELQKVLAPYARPIFLRLLPQVDTTGTFKIQ 600
Db 541 GVAVPGVEGKAGMAAVADPHSLDPAIYQELQKVLAPYARPIFLRLLPQVDTTGTFKIQ 600
QY 601 KTRLOREGFDPRTSDRLFLDLKQGHYPLNEAVYTRICSGAFAL 646
Db 601 KTRLOREGFDPRTSDRLFLDLKQGHYPLNEAVYTRICSGAFAL 646

Search completed: March 6, 2002, 13:38:48
Job time: 209 sec

Db 490 GKPCILLTKIRKNQPFGLYRG--SODETKRKLVANVRQVGDLYNTGVDLALDQEGFFYF 547
 QY 505 RDRSGDTRWRGNSVTEVEGVLRLQTDVAVYGVAVGVGKAGMAAV-ADPHSL 563
 Db 548 RDLGDTFRWKGNSVTEVEGVLRLQTDVAVYGVAVGVGKAGMAAV-ADPHSL 563
 QY 564 DPNAYQELQKVLAVYARIFIRLQVDTTGTGFKIQRKLRQEGFPDPTSDRLFLDL 623
 Db 608 DGOKLQHVRSWLPAYATPHFIRIQDSLEITNTYKLVKSQALREGFDVGIADPLYLIDN 667
 QY 624 DGOKHVLPLNEAVYTRICSGAFAL 646
 Db 668 KAETFRSLMPDVYQVACSTWKL 690

RESULT 15
 ID 088694
 AC 088694 PRELIMINARY; PRT: 662 AA.
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE FATTY ACID TRANSPORT PROTEIN 5 (VERY-LONG-CHAIN FATTY ACID TRANSPORT PROTEIN 5) (VERY-LONG-CHAIN ACYL-COA SYNTHETASE RELATED SLC27A5 OR VLACS).

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98337965; PubMed=9671728;
 RA Hirsch D., Stahl A., Lodish H.F.;
 RT "A family of fatty acid transporters conserved from mycobacterium to man.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8625-8629(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=LIVER;
 RX MEDLINE=98308102; PubMed=9642112;
 RA Berger J., Truppe C., Neumann H., Forss-Petter S.;
 RT "A novel relative of the very-long-chain acyl-CoA synthetase and fatty acid transporter protein genes with a distinct expression pattern.";
 RL Biochem. Biophys. Res. Commun. 247:255-260(1998).
 CC -!- FUNCTION: INVOLVED IN TRANSLLOCATION OF LONG-CHAIN FATTY ACIDS ACROSS THE PLASMA MEMBRANE. MAY PLAY A PIVOTAL ROLE IN REGULATING AVAILABLE LONG-CHAIN FATTY ACID SUBSTRATES FROM EXOGENOUS SOURCES IN TISSUES UNDERGOING HIGH LEVELS OF BETA-OXIDATION OR TRIGLYCERIDE SYNTHESIS.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PLASMA MEMBRANE.
 CC -!- TISSUE SPECIFICITY: LIVER, BUT NOT IN FETAL LIVER. LOW LEVELS IN BRAIN, LUNG, TESTES, SPLEEN, AND SKELETAL MUSCLE.
 CC -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
 DR EMBL; AF072760; AAC40189.1;
 DR EMBL; AJ223959; CAAL1688.1; ALT_INT.
 DR MGD; MGI:1347100; SLC27A5.
 DR InterPro; IPR000873; AMP-bind.
 DR Pfam; PF00501; AMP-binding; 1.
 DR PROSITE; PS00455; AMP_BINDING; 1.
 KW Glycoprotein; Lipid transport; Transmembrane; Signal; Transport.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 662 FATTY ACID TRANSPORT PROTEIN 5.
 FT TRANSMEM 28 48 POTENTIAL.
 FT TRANSMEM 156 175 POTENTIAL.
 FT TRANSMEM 312 332 POTENTIAL.
 FT CARBOHYD 533 533 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 1 1 M -> GWIKLTLTLLLLLVGLGQPPWPAAM (IN REF. 2).
 FT CONFLICT 61 61 K -> I (IN REF. 2).
 FT CONFLICT 381 381 T -> N (IN REF. 2).
 FT CONFLICT 541 541 C -> S (IN REF. 2).

FT CONFLICT 661 661 N -> K (IN REF. 2).
 SQ SEQUENCE 662 AA; 73251 MW; 1D7BAFE29F6D2712 CRC64;

Query Match 29.0%; Score 977.5; DB 11; Length 662;
 Best Local Similarity 37.5%; Pred. No. 6e-66;
 Matches 259; Conservative 104; Mismatches 243; Indels 85; Gaps 20;

QY 12 VSLALLW-----LLGLPW--TWS-----AAAALGVVY---GSGGWREL- 44
 Db 1 MALALRWELGDPCTCLVLLGLALLGRPWISSWMPHLSLVAALTLFLPPLPPGRLWLH 60
 QY 45 RIVCKTARRDLFGLSVLRVLRRLRRHORAGHTIPRIFQAVQVORQ-----PERALVDAGT 100
 Db 61 KDVAFTEKMLFYGL---KFRRLNKH-----PETVDALERQALADPDRVALVCTGS 110
 QY 101 -GECWTAQLDAYS-----NAVANLFRQLGFAPGDVVAIFL--EGRPEVGLW 145
 Db 111 EGSSITNSQLDARSCQAAMVLAALKAKLDAVIONTR-----DAAALVLPSTISALSVF 163
 QY 146 LGLAKAGMEALLNVLNRLRREPLAFCLGTSCAKALIFGGEWAAVAEVSCH-LGKSLIKPC 204
 Db 164 LGLAKLGPVAVINPHSRGMPLLHSYRSSGASVLIIVDPDLQENLEEVLPKLAENIHCFY 223
 QY 205 SGDLGPBGIPLDHLPLKKEASTPL-----AQIPSKGMDRLFYITSGTGLPKAA 259
 Db 224 LGHSSP---TPGVEALGASLDAAPSDVPASLRATIKWK---SPAIFITSGTGLPKPA 277
 QY 260 IVVHSRYRMA---AFGHAYRMQAADVLYDCLPLYHSAGNIIGVQCCLLYGLTVVLRKK 316
 Db 278 ILSHERVIOVNVLSF---CCRRADDVYDVLPLYHTIGLVGLGLOVGCATCVLAPK 333
 QY 317 FSASRWDDCIKYNTVQVYIGECRYLLKQPVREARRHRVRLAVGNGLRPAIWEFTE 376
 Db 334 FSASRFAECRQHGVTIVLYGELRLYLCNVPEQPEDKIHTVRLAMGTGLRANVKNFQQ 393
 QY 377 RFGVRQIGEFYGATECNCISIANMDGKVGSCGFNSRILPHYPIRLVKVNETDMELLRDAQ 436
 Db 394 REGPIRIWEFYGSTEGVGLMNYVGHCGAVGRTSCILRLMTPFELVQDIETAEPLRDKQ 453
 QY 437 GLCIPCOAGEPGLLVGINQODPLRRFDGVYVESATSKIAHSVFSKSDSAYLSGLDVLVM 496
 Db 454 GFCIPVEPKPGLLTVKRNQNPFLGYRG--SQAESNRKLVANVRVGGDYFFNGDVLTL 511
 QY 497 DELGYMYFRSDGDTFRWRGENVSTTEGVLSRLQTDVAVYGVAVGVGKAGMAAV 556
 Db 512 DQEGFFYQDRGLGDTFRWKGNSVTEVEGVLRLQTDVAVYGVAVGVGKAGMAAV 571
 QY 557 -ADPHSLDPMAYIOELQKVLAVYARIFIRLQVDTTGTGFKIQRKLRQEGFPDPTSD 615
 Db 572 KLAPGKTFDGOKLYOHRVRSWLPAYATPHFIRIQDSLEITNTYKLVKSRLVRGFDVGIIA 631
 QY 616 DRLFFDLKOGHYLPLNEAVYTRICSGAFAL 646
 Db 632 DPLYLIDNKAQTFRSLMPDVYQVACSTWNL 662

Search completed: March 6, 2002, 13:42:04
 Job time: 215 sec

QY 616 DPLFFDLKQGHVLPNEAVYTRICSGAFAL 646
 Db 606 DPLYFRPAKG-YVKITTKICAKIEGGFRLL 635

RESULT 13
 QY9Y2P5 PRELIMINARY; PRT; 690 AA.
 AC Q9Y2P5;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE VERY LONG-CHAIN ACYL-COA SYNTHETASE HOMOLOG 2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Steinberg S.J., Wang S.J., Watkins P.A.;
 RT "Human Very Long-Chain Acyl-CoA Synthetase Homolog 2.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF064255; AAD29444.1;
 DR InterPro; IPRO00873; AMP-bind.
 DR Pfam; PF00501; AMP-binding; 1.
 DR PROSITE; PS00455; AMP_BINDING; 1.
 SQ SEQUENCE 690 AA; 75384 MW; 011313424D794546 CRC64;

Query Match 29.98; Score 1007.5; DB 4; Length 690;
 Best Local Similarity 38.28; Pred. No. 3.3e-68;
 Matches 261; Conservative

QY 12 VSLALLWLLG-----LPW--TW-----SAAALGVVSGS----GHRFLR 45
 Db 29 VALTLRWLLGDPCTCCVLLGLAMLRPWPVPHGLSLAAALALTLLPARLPGLRWLL- 87
 QY 46 IVCKTARDLFGLSVLRLELR--RHORAGHTIPRIFOAVVQORPERLALVDAGTGE- 102
 Db 88 -----PADVIPFLAKILHLGLKIRCLSRQPPDFVDAFERARAOQGRALLVYTPGGAG 141
 QY 103 CWTFAOLDAYS--NAVANFLROLG-----FAPGDVVAIFL---EGRPEVGLWGLAKAGME 154
 Db 142 SVTFGELDARACQAAWALKAEGLDPASLCAGEPTALLVASQVAPALC-MWLGLAKGCP 200
 QY 155 AALLNVNLRREPLAFCLGTSGAKALIFGEMVAVAEVSGLKSLIK-FCSGDLGPEGI 213
 Db 201 TAWINPHGRGMPLAHVSLSSGARVLVDPDLRESLEELPKLQAEINRCFVLSHTSP--- 257
 QY 214 LPDTHLLDPLLKKEASTAPLAQIPSKGMDR--LFYIYTSGETGLPKAAIVVHSRYMAA 271
 Db 258 TPGVGALGAALDRAAPSHPPADLRAGITWRSPALFIYTSGETGLPKPAILTHERVLQMS- 316
 QY 272 FGHAYRRA-----QAADVLYDCLPLYHSAGNIGVGOCILGLTVLWKKFSAASRWDD 325
 Db 317 -----KMLSLGATADDVYTVPLVHYHVGVLGCLDGLGATCVLAPKFEISTCFWDD 370
 QY 326 CIKYNCTVVOYIGEICRYLLKQPVREAERHRVRLAVGNLRPAIWEETFERFVRQIGE 385
 Db 371 CRQGVTVILYVGLLRYLGNIFQPPEDRTHTVRLAMGNGLRADVWETFOORFGPIRWE 430
 QY 386 FYGATENCSTIANMDKVGCGFNSRLPHVYPIRLVKVNEEDTMELLRDAQGLCIPQAG 445
 Db 431 VYGSTEGMGLVNVYVRCGALGKMSCLLRMLSPFELVQFDMEAAPVRDNGQFCIPVGLG 490
 QY 446 EPGLLVGQINQODPLRRFDGVYS--ESATSKIAHSVFSKGSAYLSGDVLMDELGYMYF 504
 Db 491 EPGLLLTKVVSQOP---FVGYRGPRELSERKLRNVRQSGDVYNTNGDVLAMDREGFLYF 547
 QY 505 RDRSGDTFRWGENSVTTEVGVLSRLGQTDDVAVGVAVPGVEGKAGMAAV--ADPHSL 563
 Db 548 RDRLGDTFRWGENSVTTEVGVLSVQVDFTLQOVNVYGVYVCGCGEGKVGMAAVOLAPGQTF 607

QY 564 DPNAIYOELQKVLAPYARPFIPLRLPQVDTGTGTFKIQTQLRQEGDFPQTSRDLFFDL 622
 Db 608 DGEKIQHVRANLPAYATPHFIRIQDAMEVTSTFKLMKRLVREGFNVGIVVDPLFVLDN 667
 QY 624 KQGHVLPNEAVYTRICSGAFAL 646
 Db 668 RAQSERPLTAEMYQAVCEGTWRL 690

RESULT 14
 QY9ES38 PRELIMINARY; PRT; 690 AA.
 AC QY9ES38;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE BILE ACID COA LIGASE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RA Falany C.N., Xie X., Wheeler J., Wang J., Barnes S.;
 RT "Molecular cloning and expression of rat liver bile acid CoA ligase."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF242189; AAG09770.1;
 DR InterPro; IPRO00873; AMP-bind.
 DR PROSITE; PS00455; AMP_BINDING; 1.
 DR KW
 SQ SEQUENCE 690 AA; 76265 MW; D5BE8B31758DA59 CRC64;

Query Match 29.5%; Score 993.5; DB 11; Length 690;
 Best Local Similarity 37.9%; Pred. No. 3.9e-67;
 Matches 259; Conservative 101; Mismatches 258; Indels 65; Gaps

QY 10 SVVSLALLWLLGLP-----WTWSAAAALGVVYV---GGSGWRP 43
 Db 27 AATALALRWLFGDPTCEVLLGLAFGRPWISSWIPHLWSLAAAALTLLPPRPPPELRW 86
 QY 44 LRIVCKTARDLFGLSVLRLELRHORAGHTIPRIFOAVVQOR---PERLALVDA 98
 Db 87 LHKDVAFAFKLLFYGLN---LRRRLNRHP-----PELFVDALDQQAQAPDQVALVCT 131
 QY 99 GTGEC-WTFAOLDAYS--NAVANFLROLGFA-----PGDVVAIFLEGRP-EFVGLMWGLAK 151
 Db 137 GSEGSITNRELNAKQAAWALKAEKKEATIQEDKGATAILVLPKSKISALSVPFLGLAK 191
 QY 151 AGMEAALLNVNLRREPLAFCLGTSGAKALIFGEMVAVAEVSGLH-LGKSLIKFCSGDLG 201
 Db 197 LCCPVAVINPHSRGMPLLHSSVQSSGASVLIIVDPLOFNLEEVLPKLLAENIRCFYLGHSS 251
 QY 210 PEGILPDTHLLDPLLKKEASTAPLAQIPSK-----GMDRLFIYIYTSGETGLPKAAIVVHS 261
 Db 257 P---TPGVEALGAALDRAAPSDP---VPKLRANKWKSIPAIFYTSGETGLPKPAILSHE 311
 QY 265 RYRMAAFCHHAYRMOAADVLYDCLPLYHSAGNIGVGOCILGLTVLWKKFSAASRWDD 321
 Db 311 RVLQMSNVLSFCGR--TADDVVNVNVLPLVHSMGLVGLVGLCQLGATCVLAPKFSASRYNA 361
 QY 325 DCIKYNCTVVOYIGEICRYLLKQPVREAERHRVRLAVGNLRPAIWEETFERFVRQIG 381
 Db 370 ECRQSVTVVLYVGEVRLVLCNVPCQPEDKKHTVRFALGNGLRADVWENFQORFGPIRWE 431
 QY 385 EYFQATECNCSIANMDKVGCGFNSRLPHVYPIRLVKVNEEDTMELLRDAQGLCIPCOA 441
 Db 430 ELYGSTGVNGLMNVYVGHCGAVGKTSCTFIRMLTPELVQFDFIETAEAPVRQKQFCIPVET 491
 QY 445 GEPGLLVGQINQODPLRRFDGVYVSESATSKIAHSVFSKGSAYLSGDVLMDELGYMYF 501
 Db 548 GEPGLLVGQINQODPLRRFDGVYVSESATSKIAHSVFSKGSAYLSGDVLMDELGYMYF 551

RESULT 11

Q9BTYS Q9BTYS

ID Q9BTYS PRELIMINARY: PRT; 730 AA.

AC Q9BTYS

DT 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DE UNKNOWN (PROTEIN FOR MGC:4365).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LUNG CARCINOMA;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC003041; AA03041.1; -

SQ SEQUENCE 730 AA; 78644 MW; E8CC4E9463A534A0 CRC64;

Query Match

Best Local Similarity 32.1%; Score 1082; DB 4; Length 730;

Matches 253; Conservative 85; Mismatches 227; Indels 58; Gaps 12;

QY 65 RLELRHQRAGHTI-----PRFQAVVQPERIALV-----DAGT 100

Db 117 RLAELQRAAHTFLHNGSRFRYSSEARERNAARAFRALGWDGPDGDSGEGSAGE 176

QY 101 GEWTFPAQLDAYSNANVLFQGLFA-----PGDVATFLGSEFEVGLWGLAK 150

Db 177 GERAPAGDAAAGSAGFAEAGGGAARGGAARPLSPGATVALLPAGFEFLWFLGAK 236

QY 151 AGMEALLNNLRREPLACLTGSGAKALIFGEMVAAY-AEYSGHLGSLKFKSGDLG 209

Db 237 AGLTAFVPTALRRGPELLHCLSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAG--- 293

QY 210 PEGILPDTHL--LDPLLEKASTAPLAQIPS-----KGMDRLFYITSGTGLPKAAIVV 262

Db 294 -----PGTHPAGISDLLAEVSAEVDGVPVGYLSSPQSITDCLYFTSGTGLPKAAIRIS 348

QY 263 HSRYYRMAAFHHAYRMAQADVLYDCLPLYHSAGNIIGVQCILYGLTVLRLKFSASRF 322

Db 349 HLKILQCGF-YOLCGVHOEDVYILALPLYHMSGSLGIVGCMGIGATVWLKSFSAQGF 407

QY 323 WDCIKYNTVQVYIGEICRYLLKOPVREARRHRVAVGLVGLVGLVGLVGLVGLVGLV 382

Db 408 WEDCQHQHVTYVQYIGELCRYLVNPPSKAERGHKRVAVGSLRDPDWERFVRFGPLQ 467

QY 383 IGEFYGATECNCSIANMDGKVGSGFNSRILPHVYPIRLVKVNETMELLDAQGLCIPC 442

Db 468 VLETYGLTEGNVATINYTGQAVGRASWLYKHIFPFESLIRYDVTGPIRDPQGHCMAT 527

QY 443 QAGEPGLLVGOINQODPLRRDGGVYSESATSK-KIAHSVFSKGSAYLSGDVLYMDELGY 501

Db 528 SPGEGLLVAPVQSQSP---FLGVAGGPELAQGLKLLKDVFRPGDVFNTGDLVCDQGF 584

QY 502 MYFRDRSGDTFRWGENVSTTEVEGVLRLGOTDVAVYGVAVPGVSGKAGMAVA--DP 559

Db 585 LRFHRTGDTFRWGENVSTTEVEGVLRLGOTDVAVYGVAVPGVSGKAGMAVA--DP 644

QY 560 HSLLDPNAIYQELQKVLAPYARPIFLRLLPQVDTGTGTFKIQKTRLOREGDPPROTSLR 619

Db 645 HA-LDLMQYTHVSENLPYARPIFLRLLPQVDTGTGTFKIQKTRLOREGDPPROTSLR 703

QY 620 FLDLKQGHYLPNEAVYTRICSG-642

Db 704 VLDQAVGAYLPLTARYSALLAG 726

RESULT 12

Q9A5Z8

ID Q9A5Z8

AC Q9A5Z8

DT 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DE FATTY ACID TRANSPORT PROTEIN, PUTATIVE.

GN CC2239.

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;

OC Caulobacter.

OX NCBI_TaxID=69394;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21173698; PubMed=11259647;

RA Nierman J.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

RA Eisen J., Heidelberg J.F., Alley M.R.K., Onta N., Maddock J.R.,

RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Barry K.,

RA Utterback T., Iran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

RT "Complete genome sequence of Caulobacter crescentus.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

DR EMBL; AE005900; AAK24270.1; -

DR TIGR; CC2299; -

KW Complete proteome.

SQ SEQUENCE 635 AA; 71026 MW; A2AAFE1C2C150EAE CRC64;

Query Match

Best Local Similarity 30.2%; Score 1017.5; DB 2; Length 635;

Matches 243; Conservative 94; Mismatches 249; Indels 45; Gaps 13;

QY 48 CKTARD-----LFGSLVLRVLELRHRQ-----AGHTIPRI----- 81

Db 18 CSTRLRDRSGPLOWLLPRERRMLRQIKRIEFLKSLTKRVKTIAPDSNLCDD 77

QY 82 FOAVVQPERIALVDAGTGCWTFAGLDVAVNAVALFQGLFAGPDVVAIFLEGREF 141

Db 78 LEAAVDKNGPRPAI--TFEGKTIYADLDAMANYAHWAKGLGLTRGQTVLAFMPNRIEY 135

QY 142 VGLWGLAKAGMEALLNNLRREPLACLTGSCAKALIFGEMVAAYVAASVHGLGSLI 201

Db 136 LAIWYGLTKGVATALLINQLTGAALAHCLTISQAMHCIVDAETSPCFEDVKQLEHMQ 195

QY 202 KFCSGDLGPGIILPDTHLLDPLLEAS-TAPLAQIPSKM--DDRIFYITSTGTLPKA 258

Db 196 QWV---LGP--VHDDQDRLKALKSCSQLPRDRETAGELTASDTALYITSTGTLPKA 250

QY 259 AIVVHSR---YRMAAFHHAYRMAQADVLYDCLPLYHSAGNIIGVQCILYGLTVLRLK 315

Db 251 ARTHMRAQLYMRGFASTGA---KQTDRIYITPLYPYHATGGLCALGALLNGSVVLRK 307

QY 316 KFSASRFDWDCIKYNTVQVYIGEICRYLLKQPVREARRHRVRLAVGNLRLPAIWEFT 375

Db 308 KFSATHFWPDAEQCTMFYIGELCRYLANOPEHELERAHLKRLMIFGNLRADVWDDML 367

QY 376 ERFVGRQIGEFYGATECNCSIANMDGKVGSGFNSRILPHVYPIRLVKVNETMELLRDA 435

Db 368 DRFKVGDVLEFYGATEGNVSFFNFGDKRGAIRIPSYLRKKFNIRVRFDEVTETPIRG 427

QY 436 QGLCIPQAGEPGLLVGOINQODPLRRDGGVYSESATSKIAHSVFSKGSAYLSGDVILV 495

Db 428 DGCCIEAGPEEGECIGHIG-SDARSNFTGYADKAATEKKVLDHDFEKGDAWFRGDLMK 486

QY 496 MDGLGYMYFRDRSGDTFRWGENVSTTEVEGVLRLGOTDVAVYGVAVPGVSGKAGMAA 555

Db 487 VDHGDIYIFIDRIGDTFRWGENVSTTEVEGVLRLGOTDVAVYGVAVPGVSGKAGMAA 555

QY 556 VADPHSLLDPNAIYQELQKVLAPYARPIFLRLLPQVDTGTGTFKIQKTRLOREGDPPROT 615

Db 547 LVTEGD-FDLEAFAYVDEALPSYARPLFVRLQKAETGTGTFKIRKIDLVNEGDFPSKTK 605

"A family of fatty acid transporters conserved from mycobacterium to man";
Proc Natl Acad Sci U S A. 95:8625-8629(1998).
-1- FUNCTION: INVOLVED IN TRANSLLOCATION OF LONG-CHAIN FATTY ACIDS ACROSS THE PLASMA MEMBRANE. MAY PLAY A PIVOTAL ROLE IN REGULATING AVAILABLE LONG-CHAIN FATTY ACID SUBSTRATES FROM EXOGENOUS SOURCES IN TISSUES UNDERGOING HIGH LEVELS OF BETA-OXIDATION OR TRIGLYCERIDE SYNTHESIS.
-2- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PLASMA MEMBRANE.
-3- TISSUE SPECIFICITY: LUNG, LIVER, AND TESTIS.
-4- SIMILARITY: TO OTHER ENZYMS WHICH ACT VIA AN ATP-DEPENDENT COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
EMBL: AF072758; AAC40187.1; -.
MGD; MGI:1347358; SLC27a3.
InterPro: IPR000873; AMP-bind.
Pfam: PF00501; AMP-binding; 1.
PRINTS: PR00154; AMPBINDING
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Glycoprotein; Lipid transport; Transmembrane; Transport.
FT NON_TER 1 1
FT TRANSMEM 99 119 POTENTIAL.
FT TRANSMEM 262 282 POTENTIAL.
FT CARBOHYD 367 367 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 614 AA; 67041 MW; 33C2A558CDD9D989 CRC64;

Query Match 32.3%; Score 1090; DB 11; Length 614;
Best Local Similarity 40.9%; Pred. No. 1.4e-74;
Matches 247; Conservative 92; Mismatches 205; Indels 60; Gaps 11;
QY 85 VVQPERALVDAGTGEWTFQALDAYSNVANLNF-RQLGF----- 125
DB 21 LAREOPTHTFLING--AQRFSYAEARESNRIARAFTRAGWGTGRRGSGRGSTEGARV 78
QY 126 -----APGDVVALEGRPEFVGLWGLAKAGMEALLNVLNRREPLA 168
DB 79 APPAGDAARGTTAPPLAGATVALLPAGDFLWIFGLAKAGLRTAFVPTALRRGPLL 138
QY 169 FCLGTSGAKALIFGEMVAAY-AEVSGLHGLSKLIFKCSGDLPGLPDLTHL--LDPLLK 225
DB 139 HCLRCGASALVATEFELESLEPDLPALRAMGLHLWATG-----PETNVAGISNLLS 190
QY 226 EASTAPLAQIFS-----KGMDDRLFIYVTSGLTPKAAIVVHVSRYRMAAFGHAYRMQ 280
DB 191 EAADQVDEVPVGLSAPQNMIDTCLYIFTSGLTPKAAIVVHVSRYRMAAFGHAYRMQ 249
QY 281 ADVLVDCPLVHSAGNIIGVGOCLYGLTVVLRKKFSASRFDWDCIKYNTVQYIGEI 340
DB 250 QEDVIYALPLVHMSGSLGIVGCLGICATVVKPKFSASQFWDCCQKHRTVTVQYIGEL 309
QY 341 CRYLLKQPVREARRHRYLAVGNGLRPAIWEETFERFVGRIQIGEFYGATCNCISANMD 400
DB 310 CRYLVNQPPSKAEFDHKVRLAVGSLRPDTWERTFLRRFGPLQLILETYGTEGNVATFNYT 369
QY 401 GKVGSGFNRLPHVYIRLVKVNEDTWELLRDAQGLICPCOAGEPGLLVGOINQOQPL 460
DB 370 GRQAVGRASWLYKHIFPSLIRYDMVTCEPIRNAQGHMTTSPGEPGLLVAPVSQQSP- 428
QY 461 RRFDCGVSSATSK-KIAHSVFSKGDVAVLSDGLVMDDELGYMFRDRSGDTFRWRGENV 519
DB 429 --FLGAGAPELAKLKDVFWSGDFVFNFGDGLLVCEQGLFHFHDTGTIRWKGENV 486
QY 520 STTEVPELRLSGTQDVAVYVPGVEGKAGMAA-VADPHSLDDPNNAIYQELQKVLAP 578
DB 487 ATTEVAEVLTDLFQEVNIYGVTPGHEGRAGMAALRRPQALNVLQLYSHVSENLP 546
QY 579 YARPIFLRLPQVDTGTGFKIQKTRLOREGFDPQTSDFLFLDLKQGHVPLNEAVYTR 638
DB 547 YARPRELRLQESLATTETFKQKVRMANEGFDFSVLSPLLYDDQDIGAAYLPLTPARYSA 606
QY 639 ICSSG 642
DB 607 LLSG 610

RESULT 10
Q9Y2P4 PRELIMINARY; PRT; 619 AA.
ID Q9Y2P4;
AC Q9Y2P4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE VERY LONG-CHAIN ACYL-COA SYNTHETASE HOMOLOG 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN RP SEQUENCE FROM N.A.
RT Steinberg S.J., Watkins P.A.;
RT "Human Very Long-Chain Acyl-CoA Synthetase Homolog 1.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF064254; AAD29443.1; -.
DR InterPro: IPR000873; AMP-bind.
DR Pfam: PF00501; AMP-binding; 1.
DR PROSITE: PS00455; AMP_BINDING; 1.
SQ SEQUENCE 619 AA; 70111 MW; 20264CE3FB844FF5 CRC64;
Query Match 32.1%; Score 1083; DB 4; Length 619;
Best Local Similarity 37.0%; Pred. No. 4.9e-74;
Matches 243; Conservative 125; Mismatches 228; Indels 60; Gaps 14;
QY 5 GAGAAASWSALILWILGLPWTWSAAAALGVVYSGGWRFLRVICVKTARTDRDLFGLSVLIRV 64
DB 10 GAG---MVVLHFLQKLFPYFW-----DDFWFLVKV-----VLIII 42
QY 65 RLELRHQHAGH--TIPRFQAVQVQRPRLALVDAGTGECTFAQLDAYSNVANLNF-R 121
DB 43 R--LKVEYRGEVLTVLDKFLSHAKRQPKPFII--YEGDIITYQDVDRKRSRVAVFLN 98
QY 122 QLGFAFGDVVAIFLEGRPEFVGLWGLAKAGMEALLNVLNRREPLAFCLGTSGAKALIF 181
DB 99 HSELKKGDTVALMSNEPDEFVHWGLAGLCVAVPLNTNIRSNLLNCIRACGPRALVV 158
QY 182 GSEMVAAYAEVSGHLKSLIFKCSGDLPGLPDLTHLDPDLKEASTAPLAQIPSKG-- 239
DB 159 GADLGTVEILPSLSENISVWGMKDSVPQGV-----SLKEKLSSTPDEVPKSHV 211
QY 240 ---MDRLFIYVTSGLTPKAAIVVHVSRYR---MAAFGHAYRMAADVLVDCPLY 292
DB 212 VSLLKSTCLYIFTSGLTPKAAIVISQLQVLRGSVAVLWAFGCTAH-----DIVIYTLPLY 266
QY 293 HSAGNIIGVGOCLYGLTVVLRKKFSASRFDWDCIKYNTVQYIGEIFYLLKQPVREA 352
DB 267 HSSAAILIGSCVELCATCVLKKKFSASQFWSCKKYDVTVFQYIGELCRYLCKQSKREG 326
QY 353 ERRHVRVAVGNGLRPAIWEETFERFVGRIQIGEFYGATCNCISANMDKVGSCGNSRI 412
DB 327 EKQHKVRLAINGIRSDVWREFLDRFGNIKVCLEYAATSSIFSMYNTGRIGAIGRTNLF 386
QY 413 LPHVYIRLVKVNEDTWELLRDAQGLICPCOAGEPGLLVGOINQOQPLRFDGCVSE-SA 471
DB 387 YKLLSTFDLKIYDFQKDEPMRNEQGWCIHVKKGEPLLISRVNAKAP---FFGYAGPYKH 443
QY 472 TSKKIAHSVFSKGDVAVLSDGLVMDDELGYMFRDRSGDTFRWRGENVSTTEVGVLSRL 531
DB 444 TKDCLLDVFKGDDVYLVNTGDLIVQDDNFIYFDWRTGDTFRWKGENVATTEVADVIGML 503
QY 532 LGQTDVAVYVAVPGVEGKAGMAA-VADPHSLDDPNNAIYQELQKVLAPYARPIFLRLPQ 590
DB 504 DFIQEVANVYVAISYEGRAGMASIILKPNKTSLDLEKVEYVQVVTFLPAYACPRFLRQEK 563
QY 591 VDTGTGFKIQKTRLOREGFDPQTSDFLFLDLKQGHVPLNEAVYTRICSGAFAL 646
DB 564 MEATGTGFKLKHQVLEDFGPNLKIUSEPLYFMDNLKSYVLLTRELVDQIMLGEIKL 619

DE FATTY ACID TRANSPORTER PROTEIN B.
GN D1009.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Favellio T.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN TRANSLLOCATION OF LONG-CHAIN FATTY ACIDS (BY
CC SIMILARITY).
CC -1- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
DR EMBL; U40938; AAA81698.1; -;
DR HSSP; P14687; IAWU.
DR WormPep; D1009.1; CE04285.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Glycoprotein; Lipid transport; Transmembrane; Transport.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 142 162 POTENTIAL.
FT TRANSMEM 295 315 POTENTIAL.
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 655 AA; 73514 MW; 2AEB3BF7B198D14C CRC64;

Query Match 37.3%; Score 1257.5; DB 5; Length 655;
Best Local Similarity 42.4%; Pred. No. 2.7e-87;
Matches 275; Conservative 103; Mismatches 204; Indels 67; Gaps 13;

QY 34 VYVGSGWFLRI-----VCKTARDRLGLSVLRVLRLELRHQRAGHTIPRIFOAVVOR 88
DB 33 VFVGVVFLRLTDFRRALATLPDRFAGLKLILSVKSTIRGLFKKRPRIHEIFUNQVKQ 92
QY 89 OPERIALVDAGTGEWTFPAOLDAYSNANVLFRLQGLFAPGVVAIFLEGPRFVGLWGL 148
DB 93 HPNKVAIIIEGSRQLTYQELNALANQANLYVSEGYKMGDVVAFLEMENSIDFFAILWGL 152
QY 149 AKAGMEPAALLNVLNRLREPLAFCLGTSGAKALIFGGE---MVAVAEVSGLKSLIK--- 202
DB 153 SKIGVVSFAFNSNKLLEPLAHSINVSCKSCITINILLPMFKAARE-----KNLISDEI 206
QY 203 ---PCSG---DLGPEGILPDLTHLD---PLKKEASTAPLAQIPSKGMDR---LFVIYTSG 251
DB 207 HVELAGTQVDGHRHSQQDLHLFSEDEPPVI-----DGLNFRSLVLCYIYTSG 253
QY 252 TTGLPKAAIVVHSRYRMAAFGHYHARMOAADVLYDCLPLYHSAGNIIGVGQCLYIGLTV 311
DB 254 TTGNPRAVILKHPFYWIANGAGKAFGINKSDVVYITPMYHSAAGIMGSLIAFGSTA 313
QY 312 VLRRKTSASFWDCCIKYNTVVQYIGETICRYLLKQPVREARRHVRVLAGNGLRPAIW 371
DB 314 VIRKTSASFNFWDCKYKYNVTATQYIGETICRYLLAANPCPEKHNVRLMWGNLGRQIW 373
QY 372 EEFTEFGVRIQGEFYGATECNCNANMDGKVGSCGFSNRIPLHV---YPIRLVKVNETD 428
DB 374 KEFVGRGIRKIGELYGSTEGNSNIVNVDNHVGACGF-WPIYPHIGSLFVRLIKVDRA 432
QY 429 MELLRDAQGLICPCOAGEPGLLQGINQDPLRRFRFGYVSESATSKKIAHSVFSKDSAY 488
DB 433 GELERDKNGLCVCPVGETGEMVGVIKEDILKLFEGYVSEGDITAKKIYRDVFKHDKVF 492
QY 489 LSGDVLVWDELGYMFRDRSGDTFRWGENVSTTEVEGVLRLLLGQTDVANVGVAPGVE 548
DB 494 LVMDELGYMFRDRSGDTFRWGENVSTTEVEGVLRLLLGQTDVANVGVAPGVEGKAGM 553

DB 493 ASGDILLHWDLLGYLYFVDRCGDTFRWKGENVSTTEVEGILQFVMDVEDATVGVTVGKME 552
QY 549 GRAGHAA-----VADPHSILDPNATYQELQKVLAPYARPIFLRLLPQVDTTGT 596
DB 553 GRAGMAGIVVKGDTVEKFIADITSLTEN-----LASAIYPIRILCKEVDRTGT 603
QY 597 FKIQTRIQREGFD-PROTSRLFFDLKQGHYPLNEAVYTRICSGAF 644
DB 604 FLKLLKTDLOKGYDLVACKGDDPIYWSAAEKSYKPLTKMQQDIDTGVY 652

RESULT 7
Q9CV67 PRELIMINARY: PRT: 334 AA.
AC Q9CV67: (TREMREL. 17, Created)
DT 01-JUN-2001 (TREMREL. 17, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE SOLUTE CARRIER FAMILY 27 (FATTY ACID TRANSPORTER), MEMBER 4
DE (FRAGMENT).
GN SLC27A4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gofjabori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RP "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK009292; BAB26196.1; -;
DR MGD; MGI:1347347; SLC27A4.
FT NON_TER 1 1
SQ SEQUENCE 334 AA; 37868 MW; 17C085149E19BE58 CRC64;

Query Match 37.08; Score 1246; DB 11; Length 334;
Best Local Similarity 69.6%; Pred. No. 7e-87;
Matches 229; Conservative 41; Mismatches 59; Indels 0; Gaps 0;

QY 314 RKKTSASFWDCCIKYNTVVQYIGETICRYLLKQPVREARRHVRVLAGNGLRPAIWE 373
DB 2 RKKTSASFWDCCIKYNTVVQYIGELCRYLLNQPPEARESRHKVRMAGLGRQSIWTD 61
QY 374 FTERFGVRIQGEFYGATECNCNANMDGKVGSCGFSNRIPLHVPIRLVKVNETMELR 433
DB 62 FSSRPHIQVAEYFYGATECNCNANMDGKVGSCGFSNRIPLHVPIRLVKVNETMELR 121
QY 434 DAQGLICPCOAGEPGLLQGINQDPLRRFRFGYVSESATSKKIAHSVFSKDSAYLSDV 493
DB 122 GPDGVCIPQCPQGLVRIIQQDPLRRFRFGYVSEGNKIANDKFKKQDQVATGDV 181
QY 494 LVMDELGYMFRDRSGDTFRWGENVSTTEVEGVLRLLLGQTDVANVGVAPGVEGKAGM 553
DB 494 LVMDELGYMFRDRSGDTFRWGENVSTTEVEGVLRLLLGQTDVANVGVAPGVEGKAGM 553

RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,	
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	
RA	Cherry J.M., Cawley S., Dahle K., Davenport L.B., Davies P.,	
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,	
RA	Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,	
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,	
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	
RA	Liu X., Matti B., McIntosh T.C., McLeod M.P., McPherson D.,	
RA	Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,	
RA	Mount S.M., Moy M., Murphy B., Murphly L., Muzny D.M., Nelson D.L.,	
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,	
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,	
RA	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,	
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	
RA	Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,	
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	
RA	Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu H.O.,	
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,	
RT	"The genome sequence of Drosophila melanogaster."	
RL	Science 287:2185-2195(2000).	
DR	EMBL: AE003459; AAF46943.2; --	
DR	FlyBase: FBgn0034812; CG3037.	
DR	InterPro: IPR000873; AMP-bind.	
DR	Pfam: PF00501; AMP-binding; 1.	
DR	PROSITE: PS00455; AMP_BINDING; 1.	
DR	SEQUENCE 671 AA; 74780 MW; 1816C085F4309514 CRC64;	
QY	6 AGAASVSLALLWGLPWTWSA---AAALGVYVGGWRFRIKCTARRDLFLGLSVLI 62	
DB	24 APVLTATGILLYQ3-PWYGATLYAALISILLVPGHWFYIAATVTPRTVALFAYI 82	
QY	63 RVRLRRHQRAGHTTPIRFQAVVQRPRLALVDAGTGCETWTFQALDAYSANVANLFRQ 122	
DB	83 RVLLFKRQERKNLIGDIFESNVARQPKLAIV--SESQQWTFQVNEHSNRVANVFS 140	
QY	123 LGFAPGDVVAIFLEGREFVGLWGLAKAGMEALNVLNREPLAFCLGTSGAKALIFG 182	
DB	141 HGXYKGDVGLLENRAEFVATWGLGSKIGVTPLINTNLRGASQHSITVGCQTALIG 200	
QY	183 GEMVAVAEVS-----GHLGSLKFKCSGDLGPBGLPDLTHL-----LDPLLEKASTAP 231	
DB	201 ASFRSAVMDIAKDLPAHVG--LYQF--NDESNGEVASGLSGLAQQLNGLLLEAAKDK 256	
QY	232 LAQIPSKG-MDDRIFYITSGTGLPKAAIVVHSRYRMAAGHGHAYRQAADVLYDCLP 290	
DB	257 VAAGASRADHDKLVITYTSGTGLPKAAVITHSYFFIAAGHYTLGFKDQDVFFYPLP 316	
QY	291 LYHSAGNIIGVGCGLYGLTVLVRKKSFRWDDCIKYNCTVQVIGETCYRLLKQVPR 350	
DB	317 LYHTAGVMSGQALLFGSTWLRKKFSAGSYSDCAFCQCTVQVIGEMARVILATPSA 376	
QY	351 EAERRHRVLAQNGRLPAIWEETFERFGRVQIGEFYGFATCECNSTIANMDKGVSCGFNS 410	
DB	377 PHDRHQVRFVCGNGLRFPQWPQVFERGIRKVGFEYGAEGNAGNMNDSTVGAIGFTS 436	
QY	411 RILPHVTPRILVKVNETMELLDRDQGLCTPCOAGBGLLVGINOODPLRRDGGVSVES 470	
Query Match 43.8%; Score 1476.5; DB 5; Length 671;		
Best Local Similarity 47.0%; Pred. NO. 5.7e-104;		
Matches 305; Conservative 110; Mismatches 211; Indels 23; Gaps 9;		
DB	437 RILPQIYISIIIAKDPHTGTEPLRNSQGLRCEADPGVYGVKIVRGNPCREFLSYVDOK 496	
QY	471 ATSKKTAHSVSKGDSAYLSGVLVMDLGYWYFRDRSGDTFRWGENVSTVEGVLSR 530	
DB	497 ASSKKVVHVDVSKGDMAFISGDLVADERGYLYFKDRTGDFRWKGENVSTSEVEAQLSN 556	
QY	531 LIGQTDVAVYGVAVPGVEGKAGMAAVADPHSLDPAIYVQELQKVLAPYRIFIRLLPQ 590	
DB	557 LAGYKDVYGVSPINTEGRAGMAAIYDPTREVNVSQGLVELAKSLPNYARQDFLRFLRK 616	
QY	591 VDTGTGTFKQKRLQREGDFDPTQSDRLFFLDLKQCHYLPLNEAYTRI 639	
DB	617 IDLTGTGFLKRVLEQQGFPETIIDDELFAQ-PDGVYAPLTPSVTERI 664	
RESULT	4	
Q9VKU1	PRELIMINARY; PRT; 690 AA.	
AC	Q9VKU1;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	
DE	CG7400 PROTEIN.	
GN	FATP OR CG7400.	
OS	Drosophila melanogaster (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydroidea; Drosophilidae; Drosophila.	
OX	NCBI_TaxID=7227;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BERKELEY;	
RX	MEDLINE=20196006; PubMed=10731132;	
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,	
RA	Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,	
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	
RA	Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,	
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Champ M., Pfeiffer B.D.,	
RA	Aril J.F., Agbayani A., An H.-J., Nelson C.R., Miklos G.B.G.,	
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,	
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	
RA	Cherry J.M., Cawley S., Dahle K., Davenport L.B., Davies P.,	
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,	
RA	Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,	
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,	
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	
RA	Liu X., Matti B., McIntosh T.C., McLeod M.P., McPherson D.,	
RA	Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,	
RA	Mount S.M., Moy M., Murphy B., Murphly L., Muzny D.M., Nelson D.L.,	
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,	
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,	
RA	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,	
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	
RA	Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,	
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	
RA	Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu H.O.,	
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,	
RT	"The genome sequence of Drosophila melanogaster."	
RL	Science 287:2185-2195(2000).	
DR	EMBL: AE003459; AAF46943.2; --	
DR	FlyBase: FBgn0034812; CG3037.	
DR	InterPro: IPR000873; AMP-bind.	
DR	Pfam: PF00501; AMP-binding; 1.	
DR	PROSITE: PS00455; AMP_BINDING; 1.	
DR	SEQUENCE 671 AA; 74780 MW; 1816C085F4309514 CRC64;	

QY 125 FAPGDVAIFLEGRPEFVGLWGLAKAGMEAAALLNNLRREPLAFCLGTSGAKALIFGGE 184
 Db 123 LAGSDVAIAFMENREFVGLWGLMAKLGVEAALINTNLRDALLCLTTSRARALVFGSE 182
 QY 185 MVAANAESVSHLCKSLKFCSDGLGPEGLTDLPLDPLLEKEASTAPLAQIPSKGMDRL 244
 Db 183 MASAICEVHASPDPSLFCSSGWEPAVPPSTEHLDPLEKDA-PKHLPSPCDKGFTDKL 241
 QY 245 FYIYSGTGLPKAAIVVHSHRYRMAAFGHAYRMAAADVLYDCLPLYHSAAGNIIGVQC 304
 Db 242 FYIYSGTGLPKAAIVVHSHRYRMAALVYGFMRPNDDIYDCLPLYHSAAGNIIGVQC 301
 QY 305 LIYGLTVLVLRKFSASREDDCIKYNCTVQVYIGELCRYLLKQPVREARRHVRVLA 364
 Db 302 LHGTVVIRKFSASREDDCIKYNCTVQVYIGELCRYLLKQPVREARRHVRVLA 361
 QY 365 G-----LRPAI-----WEEFTFRFVRQIGEFYGEYATECNCSTANMDGVKSGCFNSRI 412
 Db 362 ASGSPSGTFFAASYPRWLSST-----GPECNCSLGNFDSQVAGCFNSRI 408
 QY 413 LPHYVPIRLVKNEDTTHLDRDAOGLCIPQAGEPGLLVGOINQDDPLRRFDGVVSESAT 472
 Db 409 LSFVPIRLVKNEDTTHLDRDAOGLCIPQAGEPGLLVGOINQDDPLRRFDGVVSESAT 468
 QY 473 SKKIAHSVFSKGSAYLSGDLVMDLGYMYFRDRSGDTRFRWGENVSTTEVEGVLSRL 532
 Db 469 NKKIADVFKGDAQYLTGDLVMDLGYMYFRDRSGDTRFRWGENVSTTEVEGVLSRL 528
 QY 533 QOTDVAIVGAVPGEVGEKAGMAAVADPHSLDPAIYQELQKVLAPYARPIFLRLPOVD 592
 Db 529 DMADVIVGVGEVGEKAGMAAVADPHSLDPAIYQELQKVLAPYARPIFLRLPOVD 588
 QY 593 TTGFVKQKTLREKAEADPAIVKTRC-SIYIERGVYVLPDQEAYSRIQAG 637
 Db 589 KTGYKQKTLREKAEADPAIVKTRC-SIYIERGVYVLPDQEAYSRIQAG 637

RESULT 2

O88562 ID O88562 PRELIMINARY; PRT; 506 AA.
 AC O88562;
 DT 01-NOV-1998 (TEMBLrel. 08, Created)
 DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DE FATTY ACID TRANSPORT PROTEIN 4 (FATP4) (LONG-CHAIN FATTY ACID
 TRANSPORT PROTEIN 4) (FRAGMENT).
 GN SLC27A4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98337965; PubMed=9671728;
 RA Hirsch D., Stahl A., Lodish H.F.;
 RT "A family of fatty acid transporters conserved from mycobacterium to
 man.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8625-8629(1998).
 CC -!- FUNCTION: INVOLVED IN TRANSLLOCATION OF LONG-CHAIN FATTY ACIDS
 ACROSS THE PLASMA MEMBRANE. MAY PLAY A PIVOTAL ROLE IN REGULATING
 AVAILABLE LONG-CHAIN FATTY ACID SUBSTRATES FROM EXOGENOUS SOURCES
 IN TISSUES UNDERGOING HIGH LEVELS OF BETA-OXIDATION OR
 TRIGLYCERIDE SYNTHESIS.
 CC -!- TISSUE SPECIFICITY: HEART, BRAIN, LUNG, LIVER, AND KIDNEY.
 CC -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
 COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
 DR EMBL; AF072759; AAC40188.1; -
 DR MGD; MGI:1347347; SLC27A4.
 DR InterPro; IPR000873; AMP-bind.
 DR Pfam; PF00501; AMP-binding; 1.
 DR PRINTS; PR00154; AMPBINDING.
 DR PROSITE; PS00455; AMP_BINDING; 1.
 KW Glycoprotein; Lipid transport; Transport.

FT NON_TER 1 1
 FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 506 AA; 56902 MW; 4EB8C0C2173326D CRC64;

Query Match 51.0%; Score 1719.5; DB 11; Length 506;
 Best Local Similarity 65.3%; Pred. No. 1.1e-122;
 Matches 324; Conservative 65; Mismatches 106; Indels 1; Gaps 1;

QY 147 GLAKAGMEAAALLNNLRREPLAFCLGTSGAKALIFGGEVAAVAVESVGHLSKLSKFCSSG 206
 Db 8 GMAKLGVAAALINTNLRDALLCLTTSRARALVFGSE 182
 QY 207 DLGPEGLPDTLHLLDPLLEKEASTAPLAQIPSKGMDRLFYIYTSGTGLPKAAIVVHSHRY 266
 Db 68 SWEPSTVPVSTEHLDPLEDA-PKHLPSHPDKGFTDKLFYIYTSGTGLPKAAIVVHSHRY 126
 QY 267 YRMAAFGHAYRMAAADVLYDCLPLYHSAAGNIIGVQCILYGLTVLVLRKFSASREDDCI 326
 Db 127 YRMAAFGHAYRMAAADVLYDCLPLYHSAAGNIIGVQCILYGLTVLVLRKFSASREDDCI 326
 QY 327 IKYNCTVQVYIGELCRYLLKQPVREARRHVRVLAQIPSKGMDRLFYIYTSGTGLPKAAIVVHSHRY 386
 Db 187 IKYNCTVQVYIGELCRYLLKQPVREARRHVRVLAQIPSKGMDRLFYIYTSGTGLPKAAIVVHSHRY 386
 QY 387 YGATECNCISANNKGVSCGPNRILPHVPIRLVKNEDTTHLDRDAOGLCIPQAGEPGLLVGO 446
 Db 247 YGATECNCISANNKGVSCGPNRILPHVPIRLVKNEDTTHLDRDAOGLCIPQAGEPGLLVGO 446
 QY 447 PGLLVGOINQDDPLRRFDGVVSESATSKKIAHSVFSKGSAYLSGDLVMDLGYMYFRDRSGD 506
 Db 307 PGLLVGOINQDDPLRRFDGVVSESATSKKIAHSVFSKGSAYLSGDLVMDLGYMYFRDRSGD 506
 QY 507 RSGDTRFRWGENVSTTEVEGVLSRLDPAIYQELQKVLAPYARPIFLRLPOVD 566
 Db 367 RSGDTRFRWGENVSTTEVEGVLSRLDPAIYQELQKVLAPYARPIFLRLPOVD 566
 QY 567 AIYQELQKVLAPYARPIFLRLPOVD 626
 Db 427 SFAQTLKKELPLYARPIFLRLPOVD 626
 QY 627 HYLPLNEAVYTRICSG 642
 Db 487 CYVALDQEAAYTRICSG 502

RESULT 3

Q9W1V9 ID Q9W1V9 PRELIMINARY; PRT; 671 AA.
 AC Q9W1V9;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DE CG3037 PROTEIN.
 GN CG3037.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1958	58.1	0	641	4	Q95186	homo sapien
2	1719.5	53.0	0	506	11	O88562	mus musculus
3	1476.5	43.8	0	671	5	Q9W1V9	Q9W1V9 drosophila
4	1348.5	40.0	0	690	5	Q9VKU1	Q9VKU1 drosophila
5	1267.5	37.6	0	650	5	Q19878	caenorhabdi
6	1257.5	37.3	0	655	5	Q18916	caenorhabdi
7	1246	37.0	0	334	11	Q9CV67	mus musculus
8	1245.5	36.9	0	661	5	Q3W185	drosophila
9	1090	32.3	0	614	11	O88561	mus musculus
10	1083	32.1	0	619	4	Q9Y2P4	homo sapien
11	1082	32.1	0	730	4	Q9BTY5	homo sapien
12	1017.5	30.2	0	635	2	Q9A5Z8	caulobacter
13	1007.5	29.9	0	690	4	Q9Y2P5	homo sapien
14	993.5	29.5	0	690	11	Q9ES38	ratu norv
15	977.5	29.0	0	662	11	O88694	mus musculus
16	915	27.1	0	258	4	Q9BTAL	homo sapien
17	899.5	26.7	0	597	2	O05307	mycobacteri
18	891	26.4	0	623	11	O88560	mus musculus
19	872	25.9	0	608	2	Q9HZV4	pseudomonas